

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In Re Application of)
David A. GOUGH and Joel R. BOCK) FOR: METHOD FOR PREDICTING
Serial No.: Unknown) PROTEIN-PROTEIN
Filed: Herewith) INTERACTIONS IN ENTIRE
) PROTEOMES
)
) Group
) Art Unit: Unknown

PRELIMINARY AMENDMENT

Commissioner for Patents
Washington, D.C. 20231

Attention: Examiner

Dear Sir:

Preliminary to the first examination of this application, please enter the following amendments:

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner for Patents, Washington, D.C. 20231 on:

November 14, 2001

(Mailing Date)

Melissa J. Leffler

(Typed Name)

(Signature)

November 14, 2001

(Date of Signature)

IN THE TITLE

Please amend the title to read:

Method for Predicting Protein Binding from Primary Structure Data.

REMARKS

The Applicants inadvertently entered the incorrect title in the Oath and Declaration and the Assignment documents. The error was not noted until after the documents were signed. Please change the title of the application to read as listed above. The Applicants certify that this change does not constitute new matter.

Respectfully submitted,

Dated: November 14, 2001

By: 

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Docket No.: 6627-PA1034

METHOD FOR PREDICTING PROTEIN(-PROTEIN INTERACTIONS IN ENTIRE PROTEOMES) BINDING DATA FROM PRIMARY STRUCTURE DATA

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

METHOD FOR PREDICTING PROTEIN BINDING FROM PRIMARY STRUCTURE DATA

CROSS-REFERENCES TO RELATED APPLICATIONS

[0001] This application claims the benefit of priority of United States provisional application Serial Number 60/248,258 filed November 14, 2001 which is incorporated herein by reference in its entirety.

COMPUTER APPENDIX

[0002] A computer program listing appendix submitted in duplicate on compact disc under § 1.52 ((e) 5) with the application is hereby incorporated by reference.

FIELD OF THE INVENTION

[0003] The invention is a trainable system and computational method for predicting the interaction of biopolymers with other biopolymers, nucleic acids, and with a variety of ligands based on the sequence or primary structure of the biomolecule.

BACKGROUND OF THE INVENTION

[0004] Determination of protein-protein interaction is a slow and cumbersome process. Methods such as the yeast two-hybrid system can reveal unexpected, transient protein-protein interactions in cells. Alternatively, more stable protein-protein interactions may be determined by immunoprecipitations and other *in vitro* binding assays. However, it is generally not possible to determine the specific sites of interaction between the proteins by these methods. High-resolution structural analysis can reveal protein-protein interactions at a molecular level. Structures can be obtained for protein complexes, but only proteins already known to interact would be studied in this manner. Pairs of proteins may be studied individually to predict protein-protein